

# SEQUENCE LISTING

<110> Thomas, Christopher  
McPherson, Michael  
Atkinson, Howard  
Neelam, Anil

<120> Plant Cell Death System

<130> 9341-028

<150> 0025225.4

<151> 2000-10-14

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 945

<212> DNA

<213> *Phytolacca americana*

<220>

<221> mutation

<222> (750)..(759)

<223> Sequence replacing removed XbaI site

<220>

<221> misc\_feature

<222> (1)..(24)

<223> Binding site for primer PPS1BF

<220>

<221> misc\_feature

<222> (736)..(777)

<223> Binding site for primer PSXDF

<220>

<221> misc\_feature

<222> Complement((735)..(776))

<223> Binding site for primer PSXDR

<220>

<221> misc\_feature

<222> Complement((922)..(945))

<223> Binding site for primer PPS2SR

<400> 1

atgaagggtga tgcttgtagt tgtgggtgacg ttaatagcgt ggctcattgc tgcaccaact 60  
tcaacttggtg ccataaatac gatcaccttt gatgctggaa atgccaccat taacaaatat 120  
gccaccttta tggaatctct tcgtaatcaa gcgaaagatc caaaactaaa atgctatggc 180  
ataccaatgc tacctgatac taattcgacc cctaagtact tattgggttaa gctccaaggt 240  
gcaaacctaa aaaccattac actaatgctg agacgaaata acttatacgt gatgggctat 300

tctgatccct tcaatggcaa taagtgtcgt taccatatat ttaatgatat tacaagcacc 360  
gaacgcactg atgtggagaa tactctttgc tcaagttcta gttctcgtgt tgcaatgtcc 420  
attaactaca atagcttata tccgaccatg gaaaagaaag cagaagtaaa ctcaagaaat 480  
caagtccaat tgggaattca aatactcagc agtgacattg gaaaaatctc tggagttgat 540  
tcattccctg taaaaactga ggcttttttt ctactggtag ccatccaaat ggtttcagag 600  
gcagcgcgat tcaagtacat agagaaccaa gtcaagacta attttaatag agcattctac 660  
cctgatccca aagtaattaa tttggaggag aagtggggca aaatctctga ggcaattcac 720  
aatgccaaaga atggggctttt acccaaacca cttgagctag tggatgccaa aggtaccaag 780  
tggatagtgc ttagagtggg tgaaatcaat cgtgatgtgg cactccttaa gtacgttaat 840  
ggaacctgtc agacaactta ccaaaatgcc atgttctctc aagttataat ttctacttat 900  
tataattata tgtctaattct tggatgatcta tttgaaggat tctaa 945

<210> 2  
<211> 314  
<212> PRT  
<213> *Phytolacca americana*

<220>  
<221> PROPEP  
<222> (1)..(24)  
<223> N-terminal processed segment

<220>  
<221> PROPEP  
<222> (287)..(314)  
<223> C-terminal processed segment

<400> 2  
Met Lys Val Met Leu Val Val Val Val Thr Leu Ile Ala Trp Leu Ile  
1 5 10 15  
Ala Ala Pro Thr Ser Thr Cys Ala Ile Asn Thr Ile Thr Phe Asp Ala  
20 25 30  
Gly Asn Ala Thr Ile Asn Lys Tyr Ala Thr Phe Met Glu Ser Leu Arg  
35 40 45  
Asn Gln Ala Lys Asp Pro Lys Leu Lys Cys Tyr Gly Ile Pro Met Leu  
50 55 60  
Pro Asp Thr Asn Ser Thr Pro Lys Tyr Leu Leu Val Lys Leu Gln Gly  
65 70 75 80  
Ala Asn Leu Lys Thr Ile Thr Leu Met Leu Arg Arg Asn Asn Leu Tyr  
85 90 95

Val Met Gly Tyr Ser Asp Pro Phe Asn Gly Asn Lys Cys Arg Tyr His  
 100 105 110  
 Ile Phe Asn Asp Ile Thr Ser Thr Glu Arg Thr Asp Val Glu Asn Thr  
 115 120 125  
 Leu Cys Ser Ser Ser Ser Ser Arg Val Ala Met Ser Ile Asn Tyr Asn  
 130 135 140  
 Ser Leu Tyr Pro Thr Met Glu Lys Lys Ala Glu Val Asn Ser Arg Asn  
 145 150 155 160  
 Gln Val Gln Leu Gly Ile Gln Ile Leu Ser Ser Asp Ile Gly Lys Ile  
 165 170 175  
 Ser Gly Val Asp Ser Phe Pro Val Lys Thr Glu Ala Phe Phe Leu Leu  
 180 185 190  
 Val Ala Ile Gln Met Val Ser Glu Ala Ala Arg Phe Lys Tyr Ile Glu  
 195 200 205  
 Asn Gln Val Lys Thr Asn Phe Asn Arg Ala Phe Tyr Pro Asp Pro Lys  
 210 215 220  
 Val Ile Asn Leu Glu Glu Lys Trp Gly Lys Ile Ser Glu Ala Ile His  
 225 230 235 240  
 Asn Ala Lys Asn Gly Ala Leu Pro Lys Pro Leu Glu Leu Val Asp Ala  
 245 250 255  
 Lys Gly Thr Lys Trp Ile Val Leu Arg Val Asp Glu Ile Asn Arg Asp  
 260 265 270  
 Val Ala Leu Leu Lys Tyr Val Asn Gly Thr Cys Gln Thr Thr Tyr Gln  
 275 280 285  
 Asn Ala Met Phe Ser Gln Val Ile Ile Ser Thr Tyr Tyr Asn Tyr Met  
 290 295 300  
 Ser Asn Leu Gly Asp Leu Phe Glu Gly Phe  
 305 310

<210> 3  
 <211> 792  
 <212> DNA  
 <213> *Phytolacca americana*

<220>  
 <221> mutation  
 <222> (612)  
 <223> Nucleotide change from published sequence

<220>  
 <221> mutation  
 <222> (681)..(686)  
 <223> Sequence replacing removed XbaI site

<220>  
 <221> misc\_feature  
 <222> (1)..(3)  
 <223> Initiation codon added via PCR primer

<220>  
 <221> misc\_feature  
 <222> (790)..(792)  
 <223> Stop codon added via PCR primer

<220>  
 <221> misc\_feature  
 <222> (1)..(29)  
 <223> Binding site for primer PS1BF

<220>  
 <221> misc\_feature  
 <222> Complement((765)..(792))  
 <223> Binding site for primer PS2SR

<220>  
 <221> misc\_feature  
 <222> Complement((436)..(462))  
 <223> Binding site for primer PS1SR

<220>  
 <221> misc\_feature  
 <222> (463)..(492)  
 <223> Binding site for primer PS2BF

<400> 3  
 atgataaata cgatcacctt tgatgctgga aatgccacca ttaacaaata tgccaccttt 60  
 atggaatctc ttcgtaatca agcgaaagat ccaaaactaa aatgctatgg cataccaatg 120  
 ctacctgata ctaattcgac ccctaagtac ttattgggta agtccaagg tgcaaaccta 180  
 aaaaccatta cactaatgct gagacgaaat aacttatacg tgatgggcta ttctgatccc 240  
 ttcaatggca ataagtgtcg ttacatata tttaatgata ttacaagcac cgaacgcact 300  
 gatgtggaga atactctttg ctcaagttct agttctcgtg ttgcaatgtc cattaactac 360  
 aatagcttat atccgaccat ggaaaagaaa gcagaagtaa actcaagaaa tcaagtccaa 420  
 ttgggaattc aaatactcag cagtgcatt ggaaaaatct ctggagttga ttcattccct 480  
 gtaaaaactg aggctttttt tctactggta gccatccaaa tggtttcaga ggcagcgca 540  
 ttcaagtaca tagagaacca agtcaagact aattttaata gagcattcta ccctgatccc 600  
 aaagtaatta acttgaggga gaagtggggc aaaatctctg aggcaattca caatgccaag 660  
 aatggggctt tacccaaacc acttgagcta gtggatgcca aaggtaccaa gtggatagtt 720  
 cttagagtgg atgaaatcaa tcgtgatgtg gcactcctta agtacgttaa tggaacctgt 780

&lt;210&gt; 4

&lt;211&gt; 263

&lt;212&gt; PRT

<213> *Phytolacca americana*

&lt;400&gt; 4

Met Ile Asn Thr Ile Thr Phe Asp Ala Gly Asn Ala Thr Ile Asn Lys  
 1 5 10 15

Tyr Ala Thr Phe Met Glu Ser Leu Arg Asn Gln Ala Lys Asp Pro Lys  
 20 25 30

Leu Lys Cys Tyr Gly Ile Pro Met Leu Pro Asp Thr Asn Ser Thr Pro  
 35 40 45

Lys Tyr Leu Leu Val Lys Leu Gln Gly Ala Asn Leu Lys Thr Ile Thr  
 50 55 60

Leu Met Leu Arg Arg Asn Asn Leu Tyr Val Met Gly Tyr Ser Asp Pro  
 65 70 75 80

Phe Asn Gly Asn Lys Cys Arg Tyr His Ile Phe Asn Asp Ile Thr Ser  
 85 90 95

Thr Glu Arg Thr Asp Val Glu Asn Thr Leu Cys Ser Ser Ser Ser Ser  
 100 105 110

Arg Val Ala Met Ser Ile Asn Tyr Asn Ser Leu Tyr Pro Thr Met Glu  
 115 120 125

Lys Lys Ala Glu Val Asn Ser Arg Asn Gln Val Gln Leu Gly Ile Gln  
 130 135 140

Ile Leu Ser Ser Asp Ile Gly Lys Ile Ser Gly Val Asp Ser Phe Pro  
 145 150 155 160

Val Lys Thr Glu Ala Phe Phe Leu Leu Val Ala Ile Gln Met Val Ser  
 165 170 175

Glu Ala Ala Arg Phe Lys Tyr Ile Glu Asn Gln Val Lys Thr Asn Phe  
 180 185 190

Asn Arg Ala Phe Tyr Pro Asp Pro Lys Val Ile Asn Leu Glu Glu Lys  
 195 200 205

Trp Gly Lys Ile Ser Glu Ala Ile His Asn Ala Lys Asn Gly Ala Leu  
 210 215 220

Pro Lys Pro Leu Glu Leu Val Asp Ala Lys Gly Thr Lys Trp Ile Val  
 225 230 235 240

Leu Arg Val Asp Glu Ile Asn Arg Asp Val Ala Leu Leu Lys Tyr Val  
 245 250 255

Asn Gly Thr Cys Gln Thr Thr  
260

<210> 5

<211> 465

<212> DNA

<213> *Phytolacca americana*

<220>

<221> misc\_feature

<222> (1)..(3)

<223> Initiation codon added via PCR primer

<220>

<221> misc\_feature

<222> (462)..(465)

<223> Stop codon added via PCR primer

<400> 5

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atgataaata cgatcacctt tgatgctgga aatgccacca ttaacaaata tgccaccttt 60
atggaatctc ttcgtaatca agcgaaagat ccaaaactaa aatgctatgg cataccaatg 120
ctacctgata ctaattcgac ccctaagtac ttattgggta agctccaagg tgcaaacta 180
aaaaccatta cactaatgct gagacgaaat aacttatacg tgatgggcta ttctgatccc 240
ttcaatggca ataagtgtcg ttaccatata tttaatgata ttacaagcac cgaacgcact 300
gatgtggaga atactctttg ctcaagttct agttctcgtg ttgcaatgtc cattaactac 360
aatagcttat atccgaccat ggaaaagaaa gcagaagtaa actcaagaaa tcaagtccaa 420
ttgggaattc aaatactcag cagtgacatt ggaaaaatct cttaa 465
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<210> 6

<211> 154

<212> PRT

<213> *Phytolacca americana*

<400> 6

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Met Ile Asn Thr Ile Thr Phe Asp Ala Gly Asn Ala Thr Ile Asn Lys
  1             5             10             15

Tyr Ala Thr Phe Met Glu Ser Leu Arg Asn Gln Ala Lys Asp Pro Lys
      20             25             30

Leu Lys Cys Tyr Gly Ile Pro Met Leu Pro Asp Thr Asn Ser Thr Pro
      35             40             45

Lys Tyr Leu Leu Val Lys Leu Gln Gly Ala Asn Leu Lys Thr Ile Thr
      50             55             60

Leu Met Leu Arg Arg Asn Asn Leu Tyr Val Met Gly Tyr Ser Asp Pro
      65             70             75             80
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Asn Gln Val Lys Thr Asn Phe Asn Arg Ala Phe Tyr Pro Asp Pro Lys  
           35                          40                          45  
 Val Ile Asn Leu Glu Glu Lys Trp Gly Lys Ile Ser Glu Ala Ile His  
           50                          55                          60  
 Asn Ala Lys Asn Gly Ala Leu Pro Lys Pro Leu Glu Leu Val Asp Ala  
           65                          70                          75                          80  
 Lys Gly Thr Lys Trp Ile Val Leu Arg Val Asp Glu Ile Asn Arg Asp  
                           85                          90                          95  
 Val Ala Leu Leu Lys Tyr Val Asn Gly Thr Cys Gln Thr Thr  
                           100                          105                          110

<210> 9  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PPS1BF primer

<220>  
 <221> misc\_feature  
 <222> (1)..(19)  
 <223> Introduced restriction sites

<400> 9  
 actcgagtct agaggattca tgaaggtgat gctttagatt gtg

43

<210> 10  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PPS2SR primer

<220>  
 <221> misc\_feature  
 <222> (1)..(19)  
 <223> Introduced restriction sites

<400> 10  
 gactagtgtc gacgagctct tagaatcctt caaatagatc acc

43

<210> 11  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence



<220>  
<223> Description of Artificial Sequence: PS1BF primer

<220>  
<221> misc\_feature  
<222> (1)..(19)  
<223> Introduced restriction sites

<400> 11  
gctcgagtct agaggattca tgataaatac gatcaccttt gatgctgg

48

<210> 12  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PS2SR primer

<220>  
<221> misc\_feature  
<222> (1)..(19)  
<223> Introduced restriction sites

<400> 12  
gactagtgtc gacgagctct taagttgtct gacaggttcc attaacg

47

<210> 13  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PS2BF primer

<220>  
<221> misc\_feature  
<222> (1)..(19)  
<223> Introduced restriction sites

<400> 13  
actcgagtct agaggatcca tgggagttga ttcattccct gtaaaaactg ag

52

<210> 14  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PS1SR primer

<220>

<221> misc\_feature  
 <222> (1)..(19)  
 <223> Introduced restriction sites  
  
 <400> 14  
 gactagtgtc gacgagctct taagagattt ttccaatgtc actgctgag 49  
  
  
 <210> 15  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PSXDF primer  
  
 <220>  
 <221> mutation  
 <222> (15)..(20)  
 <223> Nucleotides modified to remove XbaI site  
  
 <400> 15  
 gctttaccca aaccacttga gctagtggat gccaaaggta cc 42  
  
  
 <210> 16  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PSXDR primer  
  
 <220>  
 <221> mutation  
 <222> (22)..(27)  
 <223> Nucleotides modified to remove XbaI site  
  
 <400> 16  
 gtacctttgg catccactag ctcaagtggg ttgggtaaag cc 42  
  
  
 <210> 17  
 <211> 306  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Oryza sativa  
 Cystatin Delta D86 modified for potato codon usage  
  
 <400> 17  
 atgtcatcag acggaggacc agttttggga ggcgtcgaac cagttggaaa tgaaaatgat 60  
 ttgcatttgg ttgatttggc taggtttgct gttactgaac ataataaaaa agctaatagt 120

ttgttggaat ttgaaaaatt ggtagtggt aaacaacaag ttgttgctgg aactttgtac 180  
tactttacta ttgaagttaa agaaggagat gctaaaaaat tgtacgaagc taaagtttgg 240  
gaaaaacat ggatgtttta agaattgcaa gaattttaaac cagttgatgc ttcagcta 300  
gcttaa 306

<210> 18  
<211> 729  
<212> DNA  
<213> Tobacco Etch Virus

<220>  
<221> mutation  
<222> (382)..(387)  
<223> Sequence replacing the removed SpeI site

<220>  
<221> misc\_feature  
<222> (1)..(20)  
<223> Binding site for primer NIAPROSBF

<220>  
<221> misc\_feature  
<222> Complement((359)..(392))  
<223> Binding site for primer NIAPROSDR

<220>  
<221> misc\_feature  
<222> (397)..(411)  
<223> Binding site for primer NIAPROSDF

<220>  
<221> misc\_feature  
<222> Complement((709)..(729))  
<223> Binding site for primer NIAPROSR

<400> 18  
atggaaagct tgtttaagg accacgtgat tacaaccga tatcgagcac catttgtcac 60  
ttgacgaatg aatctgatgg gcacacaaca tcgttgatg gtattggatt tggtccttc 120  
atcattacaa acaagcactt gtttagaaga aataatggaa cactgttggt ccaatcacta 180  
catggtgtat tcaaggtcaa gaacaccacg actttgcaac aacacctcat tgatgggagg 240  
gacatgataa ttattcgcat gcctaaggat ttcccacat ttctcaaaa gctgaaattt 300  
agagagccac aaagggaaga ggcgatatgt cttgtgacaa ccaactcca aactaagagc 360  
atgtctagca tgggtgtcaga cacaagctgc acattccctt catctgatgg catattctgg 420  
aagcattgga ttcaaacc aa ggatgggcag tgtggcagtc cattagtatc aactagagat 480

ggggttcattg ttggtataca ctcagcatcg aatttcacca acacaaacaa ttatttcaca 540  
 agcgtgccga aaaacttcat ggaattgttg acaaatcagg aggcgcagca gtgggtagt 600  
 ggttggcgat taaatgctga ctcagtattg tggggggggcc ataaagtttt catgagcaaa 660  
 cctgaagagc cttttcagcc agttaaggaa gcgactcaac tcatgagtga attggtgtac 720  
 tcgcaataa 729

<210> 19  
 <211> 1092  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PAP-S/Cystatin  
 fusion

<220>  
 <221> misc\_feature  
 <222> (766)..(786)  
 <223> TEV NIA protease cleavage site

<220>  
 <221> mutation  
 <222> (681)..(686)  
 <223> Modified XbaI site

<220>  
 <221> misc\_feature  
 <222> (1)..(29)  
 <223> Binding site for primer PS1BF

<220>  
 <221> misc\_feature  
 <222> Complement((742)..(786))  
 <223> Binding site for primer PCS-PAPSR

<220>  
 <221> misc\_feature  
 <222> (766)..(806)  
 <223> Binding site for primer PCS-Delta86F

<220>  
 <221> misc\_feature  
 <222> Complement((1066)..(1092))  
 <223> Binding site for primer SYNPOTDelta86SR

<400> 19  
 atgataaata cgatcacctt tgatgctgga aatgccacca ttaacaaata tgccaccttt 60  
 atggaatctc ttogtaatca agcgaaagat ccaaaactaa aatgctatgg cataccaatg 120  
 ctacctgata ctaattcgac ccctaagtac ttattgggta agctccaagg tgcaaaccta 180

aaaaccatta cactaatgct gagacgaaat aacttatacg tgatgggcta ttctgatccc 240  
 ttcaatggca ataagtgtcg ttaccatata tttaatgata ttacaagcac cgaacgcact 300  
 gatgtggaga atactctttg ctcaagttct agttctcgtg ttgcaatgtc cattaactac 360  
 aatagcttat atccgaccat ggaaaagaaa gcagaagtaa actcaagaaa tcaagtccaa 420  
 ttgggaattc aaatactcag cagtgcatt ggaaaaatct ctggagttga ttcattccct 480  
 gtaaaaactg aggctttttt tctactggta gccatccaaa tggtttcaga ggagcgcgga 540  
 ttcaagtaca tagagaacca agtcaagact aattttaata gagcattcta ccctgatccc 600  
 aaagtaatta acttggagga gaagtggggc aaaatctctg aggcaattca caatgccaag 660  
 aatggggctt tacccaaacc acttgagcta gtggatgcca aaggtaccaa gtggatagtt 720  
 cttagagtgg atgaaatcaa tcgtgatgtg gcactcctta agtacgaacc agtctatttc 780  
 caagggatgt catcagacgg aggaccagtt ttgggaggcg tcgaaccagt tggaaatgaa 840  
 aatgatttgc atttggttga tttggctagg tttgctgtta ctgaacataa taaaaagct 900  
 aatagtttgt tggaatttga aaaattgggt agtggttaaac aacaagttgt tgctggaact 960  
 ttgtactact ttactattga agttaagaa ggagatgcta aaaaattgta cgaagctaaa  
 1020  
 gtttgggaaa aaccatggat gtttaaagaa ttgcaagaat ttaaaccagt tgatgcttca  
 1080  
 gctaattgct aa  
 1092

<210> 20  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCS-PAPSR  
 primer

<220>  
 <221> misc\_feature  
 <222> (1)..(21)  
 <223> TEV NIA protease cleavage site

<400> 20  
 cccttggaaa tagactgggt cgtacttaag gagtgccaca tcacg

45

<210> 21  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCS-Delta86F  
primer

<220>  
<221> misc\_feature  
<222> (1)..(21)  
<223> TEV NIA protease cleavage site

<400> 21  
gaaccagtct atttccaagg gatgtcatca gacggaggac c

41

<210> 22  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
SYNPOTDelta86SR primer

<220>  
<221> misc\_feature  
<222> (1)..(19)  
<223> Introduced restriction sites

<400> 22  
aactagtgtc gacgagctct taagcattag ctgaagcatc aactgg

46

<210> 23  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NIAPROBF  
primer

<220>  
<221> misc\_feature  
<222> (1)..(19)  
<223> Introduced restriction sites

<400> 23  
gctcgagtct agaggatcca tggaaagctt gtttaagg

39

<210> 24  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NIAPROSR

<220>  
<221> misc\_feature  
<222> (1)..(18)  
<223> Introduced restriction sites

<400> 24  
actagtgtcg acgagctctt attgcgagta caccaattc

39

<210> 25  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NIAPROSDF  
primer

<220>  
<221> mutation  
<222> (6)..(11)  
<223> Nucleotides modified to remove SpeI site

<400> 25  
cagacacaag ctgcacattc ctttcatctg atggc

35

<210> 26  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NIAPROSDR

<220>  
<221> mutation  
<222> (6)..(11)  
<223> Nucleotides modified to remove SpeI site

<400> 26  
gtgcagcttg tgtctgacac catgctagac atgc

34

<210> 27  
<211> 381  
<212> DNA  
<213> Nicotiana tabacum

<400> 27  
tctagaaagc ttatctaaac aaagttttta attcatttct taaacgtcca ttacaatgta 60

atataactta gtcgtctcaa ttaaaccatt aatgtgaaat ataaatcaaa aaaagccaaa 120  
 gggcggtggg acggcgccaa tcatttgccc tagtccactc aaataaggcc catggtcggc 180  
 aaaaccaaac acaaaatgtg ttatttttaa ttttttctc ttttattgtt aaagttgcaa 240  
 aatgtgttat ttttggttaag accctatgga tatataaaga caggttatgt gaaacttgga 300  
 aaaccatcaa gttttaagca aaaccctctt aagaacttaa attgagcttc ttttggggca 360  
 tttttctagt gagaaggatc c 381

<210> 28  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: TEV NIA  
 protease cleavage site (i)

<400> 28  
 Glu Xaa Xaa Tyr Xaa Gln Gly  
 1 5

<210> 29  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: TEV NIA  
 protease cleavage site (ii)

<400> 29  
 Glu Xaa Xaa Tyr Xaa Gln Ser  
 1 5

<210> 30  
 <211> 1379  
 <212> DNA  
 <213> Phytolacca americana

<400> 30  
 ctatgaagtc gggctcaaagc atatacaggc tatgcattgt tagaaacatt gatgcctctg 60  
 atccccgataa acaatacaaa ttagacaata agatgacata caagtaccta aactgtgtat 120  
 ggggggagtga aacctcagct gctaaaaaaa cgttgtaaga aaaaaagaaa gttgtgagtt 180  
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